RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/583,093 A

Source: IFWP

Date Processed by STIC: 5/2/07

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IFWP

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          RAW SEQUENCE LISTING                    DATE: 02/02/2007
          PATENT APPLICATION:  US/10/583,093A     TIME: 11:53:20

          Input Set : A:\MERK3179.APP
          Output Set: N:\CRF4\02022007\J583093A.raw

 3 <110> APPLICANT: FIEBIG, HELMUT
 4        NANDY, ANDREAS
 5        CROMWELL, OLIVER
 7 <120> TITLE OF INVENTION: DNA SEQUENCE, AND RECOMBINANT PREPARATION OF THE GRASS
 8        POLLEN ALLERGEN LOL P 4
10 <130> FILE REFERENCE: MERCK-3179
12 <140> CURRENT APPLICATION NUMBER: 10/583,093A
13 <141> CURRENT FILING DATE: 2006-06-15
15 <150> PRIOR APPLICATION NUMBER: PCT/EP04/013663
16 <151> PRIOR FILING DATE: 2004-12-01
18 <150> PRIOR APPLICATION NUMBER: DE 103 59 352.7
19 <151> PRIOR FILING DATE: 2003-12-16
21 <160> NUMBER OF SEQ ID NOS: 27
23 <170> SOFTWARE: PatentIn Ver. 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1272
27 <212> TYPE: DNA
28 <213> ORGANISM: Lolium perenne
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31 <221> NAME/KEY: CDS
32 <222> LOCATION: (2)..(1270)
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37   1               5                   10                  15
39 ggc ggg cac gac tac gag ggc ctc tcg tac cgc tcc ctg cag ccc gag    97
40 Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Arg Ser Leu Gln Pro Glu
41               20                  25                  30
43 aac ttc gca gtc gtc gac ctc aac cag atg cgg gcg gtg ttg gtg gac    145
44 Asn Phe Ala Val Val Asp Leu Asn Gln Met Arg Ala Val Leu Val Asp
45           35                  40                  45
47 ggt aag gcc cgc acg gcg tgg gtc gac tcc ggc gcg cag ctc ggc gag    193
48 Gly Lys Ala Arg Thr Ala Trp Val Asp Ser Gly Ala Gln Leu Gly Glu
49       50                  55                  60
51 ctc tac tac gcc atc tcc aag tat agc cgc acg ctg gcc ttc ccg gca    241
52 Leu Tyr Tyr Ala Ile Ser Lys Tyr Ser Arg Thr Leu Ala Phe Pro Ala
53 65                  70                  75                  80
55 ggc gtt tgc ccg acc atc ggc gtg ggc ggc aac ctc gcg ggc ggc ggc    289
56 Gly Val Cys Pro Thr Ile Gly Val Gly Gly Asn Leu Ala Gly Gly Gly
57               85                  90                  95
59 ttc ggt atg ctg ctg cgc aag tac ggc atc gcc gca gag aac gtc atc    337
60 Phe Gly Met Leu Leu Arg Lys Tyr Gly Ile Ala Ala Glu Asn Val Ile
61           100                 105                 110
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63 gac gtg aag ctc gtc gac gcc aac ggc aag ctg cac gac aag aag tcc   385
64 Asp Val Lys Leu Val Asp Ala Asn Gly Lys Leu His Asp Lys Lys Ser
65         115                 120                 125
67 atg ggc gac gac cat ttc tgg gcc gtg agg ggt ggc ggc ggc gag agc   433
68 Met Gly Asp Asp His Phe Trp Ala Val Arg Gly Gly Gly Gly Glu Ser
69         130                 135                 140
71 ttc ggc atc gtg gtc tcg tgg cag gtg aag ctc ctg ccg gtg cct ccc   481
72 Phe Gly Ile Val Val Ser Trp Gln Val Lys Leu Leu Pro Val Pro Pro
73 145                 150                 155                 160
75 acg gtg acc atc ttc aag atc ccc aag tca gtc agc gag ggc gcc gtg   529
76 Thr Val Thr Ile Phe Lys Ile Pro Lys Ser Val Ser Glu Gly Ala Val
77                 165                 170                 175
79 gac atc atc aac aag tgg caa ctg gtc gcg cct caa ctt ccc gcc gac   577
80 Asp Ile Ile Asn Lys Trp Gln Leu Val Ala Pro Gln Leu Pro Ala Asp
81             180                 185                 190
83 ctc atg atc cgc atc att gcg atg ggg ccc aag gcc acg ttc gag gcc   625
84 Leu Met Ile Arg Ile Ile Ala Met Gly Pro Lys Ala Thr Phe Glu Ala
85         195                 200                 205
87 atg tac ctc ggc acc tgc aaa acc ctg acg ccg atg atg cag agc aag   673
88 Met Tyr Leu Gly Thr Cys Lys Thr Leu Thr Pro Met Met Gln Ser Lys
89         210                 215                 220
91 ttc ccc gag ctt ggc atg aac gcc tcg cac tgc aac gag atg tca tgg   721
92 Phe Pro Glu Leu Gly Met Asn Ala Ser His Cys Asn Glu Met Ser Trp
93 225                 230                 235                 240
95 atc gag tcc atc ccc ttc gtc cac ctc ggc cat agg gat tcc ctg gag   769
96 Ile Glu Ser Ile Pro Phe Val His Leu Gly His Arg Asp Ser Leu Glu
97                 245                 250                 255
99 ggc gac ctc ctc aac cgg aac aac acc ttc aag ccc ttt gcg gag tac   817
100 Gly Asp Leu Leu Asn Arg Asn Asn Thr Phe Lys Pro Phe Ala Glu Tyr
101             260                 265                 270
103 aaa tcg gac tac gtc tac gag cca ttc ccc aag agc gtg tgg gag cag   865
104 Lys Ser Asp Tyr Val Tyr Glu Pro Phe Pro Lys Ser Val Trp Glu Gln
105         275                 280                 285
107 atc ttc ggc acc tgg ctc gtg aag cct ggt gcg ggg att atg atc ttt   913
108 Ile Phe Gly Thr Trp Leu Val Lys Pro Gly Ala Gly Ile Met Ile Phe
109     290                 295                 300
111 gac ccc tac ggt gcc acc atc agc gct acc cca gaa gcg gcg acg ccg   961
112 Asp Pro Tyr Gly Ala Thr Ile Ser Ala Thr Pro Glu Ala Ala Thr Pro
113 305                 310                 315                 320
115 ttc cct cac cgc aag gga gtc ctc ttc aac atc cag tac gtc aac tac  1009
116 Phe Pro His Arg Lys Gly Val Leu Phe Asn Ile Gln Tyr Val Asn Tyr
117                 325                 330                 335
119 tgg ttc gct ccg gga gcc ggc gcc gcg ccc ttg tca tgg agc aag gaa  1057
120 Trp Phe Ala Pro Gly Ala Gly Ala Ala Pro Leu Ser Trp Ser Lys Glu
121             340                 345                 350
123 atc tac aac tac atg gag ccg tac gtg agc aag aac ccc agg cag gcc  1105
124 Ile Tyr Asn Tyr Met Glu Pro Tyr Val Ser Lys Asn Pro Arg Gln Ala
125         355                 360                 365
127 tac gcc aac tac agg gac atc gac ctc ggg agg aac gag gtg gtg aat  1153
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Input Set : A:\MERK3179.APP
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129     370             375             380
131 ggc gtc tcc acc tac agc agt ggt aag gtc tgg gga cag aaa tat ttc    1201
132 Gly Val Ser Thr Tyr Ser Ser Gly Lys Val Trp Gly Gln Lys Tyr Phe
133 385             390             395             400
135 aag ggt aac ttc gag agg ctc gcc att acc aag ggc aag gtg gat cct    1249
136 Lys Gly Asn Phe Glu Arg Leu Ala Ile Thr Lys Gly Lys Val Asp Pro
137             405             410             415
139 acg gat tac ttc agg aac gag ca                                     1272
140 Thr Asp Tyr Phe Arg Asn Glu
141             420
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145 <211> LENGTH: 423
146 <212> TYPE: PRT
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151  1               5               10              15
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154             20              25              30
156 Asn Phe Ala Val Val Asp Leu Asn Gln Met Arg Ala Val Leu Val Asp
157         35              40              45
159 Gly Lys Ala Arg Thr Ala Trp Val Asp Ser Gly Ala Gln Leu Gly Glu
160     50              55              60
162 Leu Tyr Tyr Ala Ile Ser Lys Tyr Ser Arg Thr Leu Ala Phe Pro Ala
163 65              70              75              80
165 Gly Val Cys Pro Thr Ile Gly Val Gly Gly Asn Leu Ala Gly Gly Gly
166             85              90              95
168 Phe Gly Met Leu Leu Arg Lys Tyr Gly Ile Ala Ala Glu Asn Val Ile
169             100             105             110
171 Asp Val Lys Leu Val Asp Ala Asn Gly Lys Leu His Asp Lys Lys Ser
172         115             120             125
174 Met Gly Asp Asp His Phe Trp Ala Val Arg Gly Gly Gly Gly Glu Ser
175     130             135             140
177 Phe Gly Ile Val Val Ser Trp Gln Val Lys Leu Leu Pro Val Pro Pro
178 145             150             155             160
180 Thr Val Thr Ile Phe Lys Ile Pro Lys Ser Val Ser Glu Gly Ala Val
181             165             170             175
183 Asp Ile Ile Asn Lys Trp Gln Leu Val Ala Pro Gln Leu Pro Ala Asp
184             180             185             190
186 Leu Met Ile Arg Ile Ile Ala Met Gly Pro Lys Ala Thr Phe Glu Ala
187         195             200             205
189 Met Tyr Leu Gly Thr Cys Lys Thr Leu Thr Pro Met Met Gln Ser Lys
190     210             215             220
192 Phe Pro Glu Leu Gly Met Asn Ala Ser His Cys Asn Glu Met Ser Trp
193 225             230             235             240
195 Ile Glu Ser Ile Pro Phe Val His Leu Gly His Arg Asp Ser Leu Glu
196             245             250             255
198 Gly Asp Leu Leu Asn Arg Asn Asn Thr Phe Lys Pro Phe Ala Glu Tyr
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201 Lys Ser Asp Tyr Val Tyr Glu Pro Phe Pro Lys Ser Val Trp Glu Gln
202         275              280              285
204 Ile Phe Gly Thr Trp Leu Val Lys Pro Gly Ala Gly Ile Met Ile Phe
205     290              295              300
207 Asp Pro Tyr Gly Ala Thr Ile Ser Ala Thr Pro Glu Ala Ala Thr Pro
208 305              310              315              320
210 Phe Pro His Arg Lys Gly Val Leu Phe Asn Ile Gln Tyr Val Asn Tyr
211              325              330              335
213 Trp Phe Ala Pro Gly Ala Gly Ala Ala Pro Leu Ser Trp Ser Lys Glu
214         340              345              350
216 Ile Tyr Asn Tyr Met Glu Pro Tyr Val Ser Lys Asn Pro Arg Gln Ala
217         355              360              365
219 Tyr Ala Asn Tyr Arg Asp Ile Asp Leu Gly Arg Asn Glu Val Val Asn
220     370              375              380
222 Gly Val Ser Thr Tyr Ser Ser Gly Lys Val Trp Gly Gln Lys Tyr Phe
223 385              390              395              400
225 Lys Gly Asn Phe Glu Arg Leu Ala Ile Thr Lys Gly Lys Val Asp Pro
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229              420
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234 <211> LENGTH: 1503
235 <212> TYPE: DNA
236 <213> ORGANISM: Lolium perenne
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239 <221> NAME/KEY: CDS
240 <222> LOCATION: (1)..(1503)
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245  1           5               10                  15
247 aaa gaa atc ccg ccg cgt ctg ttg tac gcg aaa tcg tcg ccg gcg tat    96
248 Lys Glu Ile Pro Pro Arg Leu Leu Tyr Ala Lys Ser Ser Pro Ala Tyr
249             20              25                  30
251 ccc tca gtc ctg ggg cag acc atc cgg aac tcg agg tgg tcg tcg ccg   144
252 Pro Ser Val Leu Gly Gln Thr Ile Arg Asn Ser Arg Trp Ser Ser Pro
253         35              40                  45
255 gac aac gtg aag ccg ctc tac atc atc acc ccc acc aac gtc tcc cac   192
256 Asp Asn Val Lys Pro Leu Tyr Ile Ile Thr Pro Thr Asn Val Ser His
257     50              55                  60
259 atc cag tct gcc gtg gtg tgc ggc cgc cgt tac gac gtc cgc atc cgc   240
260 Ile Gln Ser Ala Val Val Cys Gly Arg Arg Tyr Asp Val Arg Ile Arg
261 65              70              75                  80
263 gta cgc agc ggc ggg cac gac tac gag ggc ctc tcg tac cgc tcc ctg   288
264 Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Arg Ser Leu
265              85              90                  95
267 cag ccc gag aac ttc gca gtc gtc gac ctc aac cag atg cgg gcg gtg   336
268 Gln Pro Glu Asn Phe Ala Val Val Asp Leu Asn Gln Met Arg Ala Val
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269                100                105                110
271 ttg gtg gac ggt aag gcc cgc acg gcg tgg gtc gac tcc ggc gcg cag   384
272 Leu Val Asp Gly Lys Ala Arg Thr Ala Trp Val Asp Ser Gly Ala Gln
273           115                120                125
275 ctc ggc gag ctc tac tac gcc atc tcc aag tat agc cgc acg ctg gcc   432
276 Leu Gly Glu Leu Tyr Tyr Ala Ile Ser Lys Tyr Ser Arg Thr Leu Ala
277 .   130                135                140
279 ttc ccg gca ggc gtt tgc ccg acc atc ggc gtg ggc ggc aac ctc gcg   480
280 Phe Pro Ala Gly Val Cys Pro Thr Ile Gly Val Gly Gly Asn Leu Ala
281 145                150                155                160
283 ggc ggc ggc ttc ggt atg ctg ctg cgc aag tac ggc atc gcc gca gag   528
284 Gly Gly Gly Phe Gly Met Leu Leu Arg Lys Tyr Gly Ile Ala Ala Glu
285                165                170                175
287 aac gtc atc gac gtg aag ctc gtc gac gcc aac ggc aag ctg cac gac   576
288 Asn Val Ile Asp Val Lys Leu Val Asp Ala Asn Gly Lys Leu His Asp
289           180                185                190
291 aag aag tcc atg ggc gac gac cat ttc tgg gcc gtg agg ggt ggc ggc   624
292 Lys Lys Ser Met Gly Asp Asp His Phe Trp Ala Val Arg Gly Gly Gly
293           195                200                205
295 ggc gag agc ttc ggc atc gtg gtc tcg tgg cag gtg aag ctc ctg ccg   672
296 Gly Glu Ser Phe Gly Ile Val Val Ser Trp Gln Val Lys Leu Leu Pro
297      210                215                220
299 gtg cct ccc acg gtg acc atc ttc aag atc ccc aag tca gtc agc gag   720
300 Val Pro Pro Thr Val Thr Ile Phe Lys Ile Pro Lys Ser Val Ser Glu
301 225                230                235                240
303 ggc gcc gtg gac atc atc aac aag tgg caa ctg gtc gcg cct caa ctt   768
304 Gly Ala Val Asp Ile Ile Asn Lys Trp Gln Leu Val Ala Pro Gln Leu
305                245                250                255
307 ccc gcc gac ctc atg atc cgc atc att gcg atg ggg ccc aag gcc acg   816
308 Pro Ala Asp Leu Met Ile Arg Ile Ile Ala Met Gly Pro Lys Ala Thr
309           260                265                270
311 ttc gag gcc atg tac ctc ggc acc tgc aaa acc ctg acg ccg atg atg   864
312 Phe Glu Ala Met Tyr Leu Gly Thr Cys Lys Thr Leu Thr Pro Met Met
313           275                280                285
315 cag agc aag ttc ccc gag ctt ggc atg aac gcc tcg cac tgc aac gag   912
316 Gln Ser Lys Phe Pro Glu Leu Gly Met Asn Ala Ser His Cys Asn Glu
317      290                295                300
319 atg tca tgg atc gag tcc atc ccc ttc gtc cac ctc ggc cat agg gat   960
320 Met Ser Trp Ile Glu Ser Ile Pro Phe Val His Leu Gly His Arg Asp
321 305                310                315                320
323 tcc ctg gag ggc gac ctc ctc aac cgg aac aac acc ttc aag ccc ttt  1008
324 Ser Leu Glu Gly Asp Leu Leu Asn Arg Asn Asn Thr Phe Lys Pro Phe
325           325                330                335
327 gcg gag tac aaa tcg gac tac gtc tac gag cca ttc ccc aag agc gtg  1056
328 Ala Glu Tyr Lys Ser Asp Tyr Val Tyr Glu Pro Phe Pro Lys Ser Val
329           340                345                350
331 tgg gag cag atc ttc ggc acc tgg ctc gtg aag cct ggt gcg ggg att  1104
332 Trp Glu Gln Ile Phe Gly Thr Trp Leu Val Lys Pro Gly Ala Gly Ile
333           355                360                365
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/02/2007
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Input Set : **A:\MERK3179.APP**
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<u>**Please Note:**</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; Xaa Pos. 8

VERIFICATION SUMMARY   DATE: 02/02/2007
PATENT APPLICATION: **US/10/583,093A**   TIME: 11:53:21

Input Set : **A:\MERK3179.APP**
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L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0